

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 1877

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

CCATCCTAAT ACGACTCACT ATA 23

GGGCTCGAGC GGCCGCCCGG GCAGGTGCAG GTAGCAGTGA CCCTCTGA 71

GGCGTTTGGTGCTCCGGTAACCAACACGGCTGTAGAGCGAGTGTTGCC 119

ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAA 167

MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGlu

1 5 10 15

GAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGG 215

GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg

20 25 30

GATGAAAACGTCCATTTCAATAGGATCTTCCTGCCCACCATCTACTTC 263

AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe

35 40 45

ATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTC 311

IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal

50 55 60

ATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 359

MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu

65 70 75 80

CACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGG 407

HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp

85 90 95

GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAG 455

AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys

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100 105 110
 GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 503
 AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle
 115 120 125
 CTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTCCACGCCACC 551
 LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr
 130 135 140
 AACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 599
 AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal
 145 150 155 160
 GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 647
 GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe
 165 170 175
 GCCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATC 697
 AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle
 180 185 190
 TGTGACCGCCTTTACCCCGATAGCCTGTGGATGGTGGTGTTCATTTC 743
 CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe
 195 200 205
 CAGCATATAATGGTGGGTCTCATCCTGCCCGGCATCGTCATCCTCTCC 791
 GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer
 210 215 220
 TGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 839
 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln
 225 230 235 240
 AAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTT 887
 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe
 245 250 255
 GCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATC 935
 AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle
 260 265 270
 CTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGCAC 983
 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis
 275 280 285

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AAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTG 1031
LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu
290 295 300
AACCCCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAAAAGCTCTGCC 1079
AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla
305 310 315 320
CAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCAAGATCCTT 1127
GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu
325 330 335
TCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAA 1175
SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu
340 345 350
TCCTCCAGTTTTTCACTCCAGCTAACCCCTTATGCAAAGACTTATATAAT 1223
SerSerSerPheHisSerSer
355 359
ATATATATATATATGATAAAGAACTTTTTTATGTTACACATTTTCCAG 1271
ATATAAGAGACTGACCAGTCTTGACAGTTTTTTTTTTTTTTAATTG 1319
ACTGTTGGGAGTTTATGTTCCCTCTAGTTTTTGTGAGGTTTGAATTAAT 1367
TTATATAAATATTGTTTTTTGTTTGTTCATGTGAATGAGCGTCTAGG 1415
CAGGACCTGTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGAC 1463
TGTAAGAACTGTAGAGGAAGAACTGAACATTCCAGAATGTGTGGTAAA 1511
TTGAATAAAGCTAGCCGTGATCCTCAGCTGTTGCTGCATAATCTCTTC 1559
ATTCCGAGGAGCACCCACCCACCCACCCACCCACCCATTCTTAA 1607
ATTGTTTGGTTATGCTGTGTGATGGTTTGGTTTTTTTTTTGTTGT 1655
TGTTGTTGTTTTTTTTTCTGTAAAAGATGGCACTTAAAACCAAAGCC 1703
TGAAATGGTGGTAGAAATGCTGGGGTTTTTTTTTGTGTTGTTGTTTTT 1751
CAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1799
GTATTACATTGTTAATAAAAGTCAATGATAAACTTAAAAAAAAAAAAA 1847
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877

SEQ ID NO: 2

SEQUENCE LENGTH: 690

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

09367055.080699

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

CTG

3

Leu

1

CACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGG 51

HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp

5

10

15

GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAG 99

AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys

20

25

30

GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 147

AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle

35

40

45

CTGGCCTTCATCAGCCTGGACCGGTACCTCGGCAATTGTCCACGCCACC 195

LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr

50

55

60

65

AACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 243

AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal

70

75

80

GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 291

GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe

85

90

95

GCCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATC 339

AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle

100

105

110

TGTGACCGCCTTTACCCCGATAGCCTGTGGATGGTGGTGTTCATTC 387

CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe

115

120

125

CAGCATATAATGGTGGGTCTCATCCTGCCCGGCATCGTCATCCTCTCC 435

GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer

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130 135 140 145
 TGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 483
 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln
 150 155 160
 AAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTT 531
 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe
 165 170 175
 GCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATC 579
 AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle
 180 185 190
 CTTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAC 627
 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis
 195 200 205
 AAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTG 675
 LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu
 210 215 220 225
 AACCCCATCCTCTAT 690
 AsnProIleLeuTyr
 230

SEQ ID NO: 3
 SEQUENCE LENGTH: 685
 SEQUENCE TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

CCATCCTAATACGACTCACTATA 23
 GGGCTCGAGCGGCCCGCCGGGCAGGTGCAGGTAGCAGTGACCCTCTGA 71
 GGCGTTTGGTGCTCCGGTAACCACCACGGCTGTAGAGCGAGTGTTGCC 119
 ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAA 167
 MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGlu

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1 5 10 15
GAAGTGGGGTCTGGAGACTATGACTCCACAAGGAACCCTGCTTCCGG 215
GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg
20 25 30
GATGAAAACGTCCATTTCAATAGGATCTTGCTGCCCACCATCTACTTC 263
AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe
35 40 45
ATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTC 311
IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal
50 55 60
ATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 359
MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu
65 70 75 80
CACCTGTCAGTGGCTGACCTCCTCTTTGTTCATCACACTCCCCTTCTGG 407
HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp
85 90 95
GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAATTTTGTGTAAG 455
AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys
100 105 110
GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 503
AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle
115 120 125
CTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTCCACGCCACC 551
LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr
130 135 140
AACAGTCAAAGGCCAAGGAACTGCTGGCTGAAAAGGCAGTCTATGTG 599
AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal
145 150 155 160
GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 647
GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe
165 170 175
GCCGACGTCAGCCAGGGGACATCAGTCAGGGGGATGA 685
AlaAspValSerGlnGlyAspIleSerGlnGlyAsp
180 185

009080"25029360

SEQ ID NO: 4

SEQUENCE LENGTH: 1694

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

ATATACACTTCTGATAACTACTCTGAA 27
IleTyrThrSerAspAsnTyrSerGlu
1 5
GAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGG 75
GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg
10 15 20 25
GATGAAAACGTCCATTTCAATAGGATCTTCCTGCCCACCATCTACTTC 123
AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe
30 35 40
ATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTC 171
IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal
45 50 55
ATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 219
MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu
60 65 70
CACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGG 267
HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp
75 80 85
GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTTGTGTAAG 315
AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys
90 95 100 105
GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 363
AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle
110 115 120
CTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTGCACGCCACC 411

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LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr
 125 130 135
 AACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 459
 AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal
 140 145 150
 GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 507
 GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe
 155 160 165
 GCCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATC 555
 AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle
 170 175 180 185
 TGTGACCGCCTTTACCCCGATAGCCTGTGGATGGTGGTGTTCATTC 603
 CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe
 190 195 200
 CAGCATATAATGGTGGGTCTCATCCTGCCCGGCATCGTCATCCTCTCC 651
 GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer
 205 210 215
 TGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 699
 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln
 220 225 230
 AAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTT 747
 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe
 235 240 245
 GCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATC 795
 AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle
 250 255 260 265
 CTTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAC 843
 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis
 270 275 280
 AAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTG 891
 LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu
 285 290 295
 AACCCCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAAAGCTCTGCC 939
 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla

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300 305 310
CAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCAAGATCCTT 987
GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu
315 320 325
TCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAA 1035
SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu
330 335 340 345
TCCTCCAGTTTTTCACTCCAGCTAACCCTTATGCAAAGACTTATATAAT 1083
SerSerSerPheHisSerSer
350
ATATATATATATATGATAAAGAACTTTTTTATGTTACACATTTTCCAG 1131
ATATAAGAGACTGACCAGTCTTGACAGTTTTTTTTTTTTTTAATTG 1179
ACTGTTGGGAGTTTATGTTCCCTCTAGTTTTTGTGAGGTTTGACTTAAT 1227
TTATATAAATATTGTTTTTTGTTTGTTCATGTGAATGAGCGTCTAGG 1275
CAGGACCTGTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGAC 1323
TGTAAGAACTGTAGAGGAAGAACTGAACATTCCAGAATGTGTGGTAAA 1371
TTGAATAAAGCTAGCCGTGATCCTCAGCTGTTCTGCATAATCTCTTC 1419
ATTCCGAGGAGCACCCACCCACCCACCCACCCACCCATTCTTAA 1467
ATTGTTTGGTTATGCTGTGTGATGGTTTGTGTTTGTGTTTGTGTTGT 1515
TGTTGTTGTTTTTTTTTTCTGTAAAAGATGGCACTTAAAACCAAAGCC 1563
TGAAATGGTGGTAGAAATGCTGGGGTTTTTTTGTGTTGTTGTTTTTT 1611
CAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1659
GTATTACATTGTTAATAAAAGTCAATGATAAACTT 1694

SEQ ID NO: 5

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

FEATURE: 13, 15 (inosine)

SEQUENCE DESCRIPTION:

CTSMGTTTGK CMNTNKCYGA

SEQ ID NO: 6
SEQUENCE LENGTH: 26
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
FEATURE: 8, 9, 17 (inosine)
SEQUENCE DESCRIPTION:
TAGAKSANNG GRTTSANRCA RCAGTG 26

SEQ ID NO: 7
SEQUENCE LENGTH: 25
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
SEQUENCE DESCRIPTION:
TCATCCCCCT GACTGATGTC CCGCT 25

SEQ ID NO: 8
SEQUENCE LENGTH: 27
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
SEQUENCE DESCRIPTION:
CCATCCTAAT ACGACTCACT ATAGGCC 27

SEQ ID NO: 9
SEQUENCE LENGTH: 30
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)

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SEQUENCE DESCRIPTION:

CGCGTCGACC ACAACATGCT GTCCACATCA

30

SEQ ID NO: 10

SEQUENCE LENGTH: 30

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:

CGCTCTAGAT TATAAACCAG CCGAGACTTC

30

SEQ ID NO: 11

SEQUENCE LENGTH: 29

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:

CGCGTCGACG TTACCATGGA GGGGATCAG

29

SEQ ID NO: 12

SEQUENCE LENGTH: 32

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:

CGCGCGGCCG CTTAGCTGGA GTGAAACTT GA

32

SEQ ID NO: 13

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
SEQUENCE DESCRIPTION:
TAGCGGCCGC GTTGCCATGG AACCGAT 27

SEQ ID NO: 14
SEQUENCE LENGTH: 27
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
SEQUENCE DESCRIPTION:
GCGTCGACTA AGGGTTAGCT GGAGTGA 27

SEQ ID NO: 15
SEQUENCE LENGTH: 20
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
SEQUENCE DESCRIPTION:
CTGCACCTGT CAGTGGCTGA 20

SEQ ID NO: 16
SEQUENCE LENGTH: 27
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic DNA)
SEQUENCE DESCRIPTION:
TAGATGAGGG GGATTGAGAC AACAGTG 27

SEQ ID NO: 17
SEQUENCE LENGTH: 359

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SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGlu

1 5 10 15

GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg

20 25 30

AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe

35 40 45

IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal

50 55 60

MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu

65 70 75 80

HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp

85 90 95

AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys

100 105 110

AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle

115 120 125

LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr

130 135 140

AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal

145 150 155 160

GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe

165 170 175

AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle

180 185 190

CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe

195 200 205

GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer

210 215 220

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CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln
225 230 235 240
LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe
245 250 255
AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle
260 265 270
LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis
275 280 285
LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu
290 295 300
AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla
305 310 315 320
GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu
325 330 335
SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu
340 345 350
SerSerSerPheHisSerSer
355 359